

# SEQUENCE LISTING

<110> Synaptic Pharmaceutical Corporation

<120> DNA Encoding A Human Melanin Concentrating Hormone  
Receptor (MCH1) And Uses Thereof

<130> 57453-A-PCT/JPW

<140> PCT/US99/31169

<141> 1999-12-30

<150> 09/224,426

<151> 1998-12-31

<160> 29

<170> PatentIn Ver. 2.1

<210> .1

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 1

```

atgtcagtgg gagccatgaa gaagggagtg gggagggcag ttgggcttgg aggcggcagc 60
ggctgccagg ctacggagga agacccccct cccgactgcg gggcttgcgc tccgggacaa 120
ggtggcaggc gctggaggct gccgcagcct gcgtgggtgg aggggagctc agctcggttg 180
tgggagcagg cgaccggcac tggttgatg gacctggaag cctcgctgct gcccactggg 240
cccaatgcc a gcaacacctc tgatggcccc gataacctca cttcagcagg atcacctcct 300
cgcacgggga gcatctccta catcaacatc atcatgcctt cgggtgttcg caccatctgc 360
ctcctgggca tcatcgggaa ctccacggtc atcttcgcgg tcgtgaagaa gtccaagctg 420
cactggtgca acaacgtccc cgacatcttc atcatcaacc tctcggtagt agatctcttc 480
tttctcttgg gcatgccctt catgatccac cagctcatgg gcaatggggg gtggcacttt 540
ggggagacca tgtgcaccct catcacggcc atggatgcca atagtcagtt caccagcacc 600
tacatcctga ccgccatggc cattgaccgc tacctggcca ctgtccacc catctcttcc 660
acgaagtacc ggaagccctc tgtggccacc ctggtgatct gcctcctgtg ggccctctcc 720
ttcatcagca tcaccctgt gtggctgtat gccagactca tccccttccc aggaggtgca 780
gtgggctgcg gcatacgctt gcccaaccca gacactgacc tctactgggt caccctgtac 840
cagtttttcc tggcctttgc cctgcctttt gtggtcatca cagccgcata cgtgaggatc 900
ctgcagcgca tgacgtcctc agtggcccc gcctcccagc gcagcatccg gctgcggaca 960
aagaggggta cccgcacagc catcgccatc tgtctggtct tctttgtgtg ctgggcaccc 1020
tactatgtgc tacagctgac ccagttgtcc atcagccgcc cgaccctcac ctttgtctac 1080
ttatacaatg cggccatcag cttgggctat gccaacagct gcctcaaccc ctttgtgtac 1140
atcgtgctct gtgagacgtt ccgcaaacgc ttggtcctgt cgggtgaagcc tgcagcccag 1200
gggcagcttc gcgctgtcag caacgctcag acggctgacg aggagaggac agaaagcaaa 1260
ggcacctga
1269

```

<210> 2  
 <211> 422  
 <212> PRT  
 <213> Homo sapiens

<400> 2

```

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
  1              5              10              15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
      20              25              30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
      35              40              45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
      50              55              60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
      65              70              75              80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
      85              90              95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
      100              105              110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
      115              120              125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
      130              135              140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
      145              150              155              160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
      165              170              175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
      180              185              190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
      195              200              205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
      210              215              220

```

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
405 410 415

Thr Glu Ser Lys Gly Thr  
420

<210> 3

<211> 1214

<212> DNA

<213> Rattus norvegicus

<400> 3

gcaggcgacc tgcaccggct gcatggatct gcaaacctcg ttgctgtcca ctggcccaa 60

tgccagcaac atctccgatg gccaggataa tctcacattg ccgggggtcac ctccctcgcac 120  
 agggagtgtc tectacatca acatcattat gccttccgtg tttggtacca tctgtctcct 180  
 gggcatcgtg ggaaactcca cggtcattct tgctgtggtg aagaagtcca agctacactg 240  
 gtgcagcaac gtcccccaga tcttcatcat caacctctct gtggtggatc tgctcttctt 300  
 gctgggcatg cctttcatga tccaccagct catggggaac ggctgtctggc actttgggga 360  
 aaccatgtgc accctcatca cagccatgga cgccaacagt cagttcacta gcacctacat 420  
 cctgactgcc atgaccattg accgctactt ggccaccgtc caccocatct cctccaccaa 480  
 gttccggaag ccttccatgg ccaccctggt gatctgcctc ctgtggggcgc tctccttcat 540  
 cagtatcacc cctgtgtggc tctacgccag gctcattccc tcccagggg gtgctgtggg 600  
 ctgtggcatc cgctgccaa acccggacac tgacctctac tggttcactc tgtaccagtt 660  
 tttcctggcc tttgcccttc cgtttgtggt cattaccgcc gcatacgtga aaatactaca 720  
 ggcgatgacg tcttcggtgg cccagcctc ccaacgcagc atccggcttc ggacaaagag 780  
 ggtgaccgcg acggccattg ccattctgtt ggtcttcttt gtgtgctggg caccctacta 840  
 tgtgtctgag ctgaccgcag tgtccatcag ccgcccgaac ctacgctttg tctacttgta 900  
 caacgcggcc atcagcttgg gctatgctaa cagctgcctg aaccctttt tgtacatagt 960  
 gctctgtgag acctttcgaa aacgcttggg gttgtcagtg aagcctgcag cccaggggca 1020  
 gctccgcacg gtcagcaacg ctacagacagc tgatgaggag aggacagaaa gcaaaggcac 1080  
 ctgacaattc cccagtcgcc tccaagtcag gccaccccat caaacctggg ggagagatac 1140  
 tgagattaaa cccaaggcta ccttgggaga atgcagaggc tggaggctgg gggctttag 1200  
 caaccacatt ccac 1214

<210> 4

<211> 353

<212> PRT

<213> Rattus norvegicus

<400> 4

Met	Asp	Leu	Gln	Thr	Ser	Leu	Leu	Ser	Thr	Gly	Pro	Asn	Ala	Ser	Asn
1				5					10					15	

Ile	Ser	Asp	Gly	Gln	Asp	Asn	Leu	Thr	Leu	Pro	Gly	Ser	Pro	Pro	Arg
			20					25						30	

Thr	Gly	Ser	Val	Ser	Tyr	Ile	Asn	Ile	Ile	Met	Pro	Ser	Val	Phe	Gly
			35				40						45		

Thr	Ile	Cys	Leu	Leu	Gly	Ile	Val	Gly	Asn	Ser	Thr	Val	Ile	Phe	Ala
			50				55				60				

Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Ser	Asn	Val	Pro	Asp	Ile
			65			70					75				80

Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu	Phe	Leu	Leu	Gly	Met
				85					90					95	

Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly	Val	Trp	His	Phe	Gly
						100			105					110	

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe  
 115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala  
 130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala  
 145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr  
 165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val  
 180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe  
 195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile  
 210 215 220

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala  
 225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg  
 245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr  
 260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr  
 275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser  
 290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys  
 305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr  
 325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly  
 340 345 350

Thr

<210> 5  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 5  
gggaactcca cggtcattctt cgcggt 26

<210> 6  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 6  
tagcgggtcaa tggccatggc ggtcag 26

<210> 7  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 7  
ctcctgggca tgcccttcat gatccaccag ctcatgggca atggg 45

<210> 8  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 8  
cttctaggcc tgtacggaag tgtta 25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 9  
gttgtggttt gtccaaactc atcaatg

27

<210> 10  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 10  
cgcggtacca ttatgtctgc actccgaagg aaatttg

37

<210> 11  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 11  
cgcgaattct tatgtgaagc gatcagagtt catttttc

38

<210> 12  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 12  
gcgggatccg ctatggctgg tgattctagg aatg

34

<210> 13  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 13  
ccggaattcc cctcacaccg agccoctgg

29

<210> 14  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 14  
tcagctcggt tgtgggagca

20

<210> 15  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 15  
cttgacttc ttcacgac

18

<210> 16  
<211> 100  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 16



Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu  
1 5 10 15  
Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30  
Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45  
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60  
Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80  
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95  
Gly Ser Pro Pro  
100

<210> 17  
<211> 100  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 17  
Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15  
Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30  
Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45  
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60  
Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80  
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

Gly Ser Pro Pro  
100

<210> 18  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 18  
cggcactggc tgggcggacc tggaagcctc g 31

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 19  
cgaggcttcc aggtccgccc agccagtgcc g 31

<210> 20  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 20  
atgtcagtgg gagccgcgaa gaagggagtg gg 32

<210> 21  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 21

cccactccct tcttcgcggc tcccactgac at

32

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 22

taatgtgtct aggtggcgtc agtgggagcc atg

33

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 23

catggctccc actgacgcca cctagacaca tta

33

<210> 24

<400> 24

000

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 25

tgacactaag cttcactggc tggatggacc tggaagc

37

<210> 26

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 26  
gcccaggaga aagaggagat ctac

24

<210> 27  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 27  
Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15  
Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30  
Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45  
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60  
Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80  
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95  
Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110  
Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125  
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140

Asn	Val	Pro	Asp	Ile	Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu	145	150	155	160
Phe	Leu	Leu	Gly	Met	Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly	165	170	175	
Val	Trp	His	Phe	Gly	Glu	Thr	Met	Cys	Thr	Leu	Ile	Thr	Ala	Met	Asp	180	185	190	
Ala	Asn	Ser	Gln	Phe	Thr	Ser	Thr	Tyr	Ile	Leu	Thr	Ala	Met	Ala	Ile	195	200	205	
Asp	Arg	Tyr	Leu	Ala	Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Lys	Phe	Arg	210	215	220	
Lys	Pro	Ser	Val	Ala	Thr	Leu	Val	Ile	Cys	Leu	Leu	Trp	Ala	Leu	Ser	225	230	235	240
Phe	Ile	Ser	Ile	Thr	Pro	Val	Trp	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe	245	250	255	
Pro	Gly	Gly	Ala	Val	Gly	Cys	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr	260	265	270	
Asp	Leu	Tyr	Trp	Phe	Thr	Leu	Tyr	Gln	Phe	Phe	Leu	Ala	Phe	Ala	Leu	275	280	285	
Pro	Phe	Val	Val	Ile	Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg	Met	290	295	300	
Thr	Ser	Ser	Val	Ala	Pro	Ala	Ser	Gln	Arg	Ser	Ile	Arg	Leu	Arg	Thr	305	310	315	320
Lys	Arg	Val	Thr	Arg	Thr	Ala	Ile	Ala	Ile	Cys	Leu	Val	Phe	Phe	Val	325	330	335	
Cys	Trp	Ala	Pro	Tyr	Tyr	Val	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser	340	345	350	
Arg	Pro	Thr	Leu	Thr	Phe	Val	Tyr	Leu	Tyr	Asn	Ala	Ala	Ile	Ser	Leu	355	360	365	
Gly	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	Pro	Phe	Val	Tyr	Ile	Val	Leu	Cys	370	375	380	
Glu	Thr	Phe	Arg	Lys	Arg	Leu	Val	Leu	Ser	Val	Lys	Pro	Ala	Ala	Gln	385	390	395	400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
405 410 415

Thr Glu Ser Lys Gly Thr  
420

<210> 28  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 28  
Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15  
Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30  
Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45  
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60  
Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80  
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95  
Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110  
Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125  
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140  
Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu  
145 150 155 160  
Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly

165 170 175  
 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp  
 180 185 190  
 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile  
 195 200 205  
 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg  
 210 215 220  
 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
 225 230 235 240  
 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
 245 250 255  
 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
 260 265 270  
 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
 275 280 285  
 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
 290 295 300  
 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
 305 310 315 320  
 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
 325 330 335  
 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
 340 345 350  
 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
 355 360 365  
 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
 370 375 380  
 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
 385 390 395 400  
 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
 405 410 415  
 Thr Glu Ser Lys Gly Thr

&lt;210&gt; 29

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: mutated human  
MCH1

&lt;400&gt; 29

Met	Asp	Leu	Glu	Ala	Ser	Leu	Leu	Pro	Thr	Gly	Pro	Asn	Ala	Ser	Asn
1				5					10					15	

Thr	Ser	Asp	Gly	Pro	Asp	Asn	Leu	Thr	Ser	Ala	Gly	Ser	Pro	Pro	Arg
			20					25					30		

Thr	Gly	Ser	Ile	Ser	Tyr	Ile	Asn	Ile	Ile	Met	Pro	Ser	Val	Phe	Gly
		35					40					45			

Thr	Ile	Cys	Leu	Leu	Gly	Ile	Ile	Gly	Asn	Ser	Thr	Val	Ile	Phe	Ala
	50					55					60				

Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Asn	Asn	Val	Pro	Asp	Ile
	65				70					75					80

Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu	Phe	Leu	Leu	Gly	Met
			85						90					95	

Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly	Val	Trp	His	Phe	Gly
		100						105					110		

Glu	Thr	Met	Cys	Thr	Leu	Ile	Thr	Ala	Met	Asp	Ala	Asn	Ser	Gln	Phe
		115					120					125			

Thr	Ser	Thr	Tyr	Ile	Leu	Thr	Ala	Met	Ala	Ile	Asp	Arg	Tyr	Leu	Ala
	130					135					140				

Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Lys	Phe	Arg	Lys	Pro	Ser	Val	Ala
145					150					155					160

Thr	Leu	Val	Ile	Cys	Leu	Leu	Trp	Ala	Leu	Ser	Phe	Ile	Ser	Ile	Thr
				165				170						175	

Pro	Val	Trp	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe	Pro	Gly	Gly	Ala	Val
			180					185					190		



Gly	Cys	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr	Asp	Leu	Tyr	Trp	Phe	195	200	205
Thr	Leu	Tyr	Gln	Phe	Phe	Leu	Ala	Phe	Ala	Leu	Pro	Phe	Val	Val	Ile	210	215	220
Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg	Met	Thr	Ser	Ser	Val	Ala	225	230	235
Pro	Ala	Ser	Gln	Arg	Ser	Ile	Arg	Leu	Arg	Thr	Lys	Arg	Val	Thr	Arg	245	250	255
Thr	Ala	Ile	Ala	Ile	Cys	Leu	Val	Phe	Phe	Val	Cys	Trp	Ala	Pro	Tyr	260	265	270
Tyr	Val	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser	Arg	Pro	Thr	Leu	Thr	275	280	285
Phe	Val	Tyr	Leu	Tyr	Asn	Ala	Ala	Ile	Ser	Leu	Gly	Tyr	Ala	Asn	Ser	290	295	300
Cys	Leu	Asn	Pro	Phe	Val	Tyr	Ile	Val	Leu	Cys	Glu	Thr	Phe	Arg	Lys	305	310	315
Arg	Leu	Val	Leu	Ser	Val	Lys	Pro	Ala	Ala	Gln	Gly	Gln	Leu	Arg	Ala	325	330	335
Val	Ser	Asn	Ala	Gln	Thr	Ala	Asp	Glu	Glu	Arg	Thr	Glu	Ser	Lys	Gly	340	345	350
Thr																		